RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/812,315

Source: PF WO

Date Processed by STIC: 4/6/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
      http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 10/812,315

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 _____ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering use space characters, instead.

4 _____ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug" sequences(s) _____ . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.

7 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:(insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped _____

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(NEW RULES) <210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _V_ Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence.

11 _____ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

```
        RAW SEQUENCE LISTING                    DATE: 04/06/2004
        PATENT APPLICATION:  US/10/812,315      TIME: 10:51:23

        Input Set : A:\Sequence Listing 81000.txt
        Output Set: N:\CRF4\04062004\J812315.raw

     4 <110> APPLICANT: Degussa AG
     6 <120> TITLE OF INVENTION: A process for producing L-amino acids using strains of the
     7       Enterobacteriaceae family
     9 <130> FILE REFERENCE: 020481 BT
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/812,315
C--> 11 <141> CURRENT FILING DATE: 2004-03-30
    11 <160> NUMBER OF SEQ ID NOS: 4
    13 <170> SOFTWARE: PatentIn version 3.1
    15 <210> SEQ ID NO: 1
    16 <211> LENGTH: 32
    17 <212> TYPE: DNA
    18 <213> ORGANISM: Synthetic sequence
    21 <220> FEATURE:
W--> 22 <221> NAME/KEY: Primer
    23 <222> LOCATION: (1)..(32)
    24 <223> OTHER INFORMATION: galP1
    27 <400> SEQUENCE: 1
    28 cacaatctag ataaaccata ttggagggca tc                             32
    30 <210> SEQ ID NO: 2
    31 <211> LENGTH: 25
    32 <212> TYPE: DNA
    33 <213> ORGANISM: Synthetic sequence
    36 <220> FEATURE:
W--> 37 <221> NAME/KEY: Primer
    38 <222> LOCATION: (1)..(25)
    39 <223> OTHER INFORMATION: galP2
    42 <400> SEQUENCE: 2
    43 gggaggaagc ttggggagat taatc                                     25
    45 <210> SEQ ID NO: 3
    46 <211> LENGTH: 1446
    47 <212> TYPE: DNA
    48 <213> ORGANISM: Escherichia coli
    51 <220> FEATURE:
W--> 52 <221> NAME/KEY: DNA fragment
    53 <222> LOCATION: (1)..(1446)
    54 <223> OTHER INFORMATION: PCR product
    57 <220> FEATURE:
    58 <221> NAME/KEY: CDS
    59 <222> LOCATION: (33)..(1427)
    60 <223> OTHER INFORMATION: galP coding region
W--> 61 <400> SEQUENCE: 3
    62 cacaatctag ataaaccata ttggagggca tc atg cct gac gct aaa aaa cag   53
    63                                    Met Pro Asp Ala Lys Lys Gln
```

Handwritten annotations: Invalid Response, Does Not Comply, Corrected Diskette Needed (Pg.1); <213> has to be either Artificial/unknown OR Genus/Species. Invalid Response, same error. Please see item #10 on error summary sheet.

```
64                                      1              5
66 ggg cgg tca aac aag gca atg acg ttt ttc gtc tgc ttc ctt gcc gct      101
67 Gly Arg Ser Asn Lys Ala Met Thr Phe Phe Val Cys Phe Leu Ala Ala
68          10                  15                  20
70 ctg gcg gga tta ctc ttt ggc ctg gat atc ggt gta att gct ggc gca      149
71 Leu Ala Gly Leu Leu Phe Gly Leu Asp Ile Gly Val Ile Ala Gly Ala
72          25                  30                  35
74 ctg ccg ttt att gca gat gaa ttc cag att act tcg cac acg caa gaa      197
75 Leu Pro Phe Ile Ala Asp Glu Phe Gln Ile Thr Ser His Thr Gln Glu
76 40                  45                  50                  55
78 tgg gtc gta agc tcc atg atg ttc ggt gcg gca gtc ggt gcg gtg ggc      245
79 Trp Val Val Ser Ser Met Met Phe Gly Ala Ala Val Gly Ala Val Gly
80                  60                  65                  70
82 agc ggc tgg ctc tcc ttt aaa ctc ggg cgc aaa aag agc ctg atg atc      293
83 Ser Gly Trp Leu Ser Phe Lys Leu Gly Arg Lys Lys Ser Leu Met Ile
84          75                  80                  85
86 ggc gca att ttg ttt gtt gcc ggt tcg ctg ttc tct gcg gct gcg cca      341
87 Gly Ala Ile Leu Phe Val Ala Gly Ser Leu Phe Ser Ala Ala Ala Pro
88          90                  95                  100
90 aac gtt gaa gta ctg att ctt tcc cgc gtt cta ctg ggg ctg gcg gtg      389
91 Asn Val Glu Val Leu Ile Leu Ser Arg Val Leu Leu Gly Leu Ala Val
92          105                 110                 115
94 ggt gtg gcc tct tat acc gca ccg ctg tac ctc tct gaa att gcg ccg      437
95 Gly Val Ala Ser Tyr Thr Ala Pro Leu Tyr Leu Ser Glu Ile Ala Pro
96 120                 125                 130                 135
98 gaa aaa att cgt ggc agt atg atc tcg atg tat cag ttg atg atc act      485
99 Glu Lys Ile Arg Gly Ser Met Ile Ser Met Tyr Gln Leu Met Ile Thr
100                 140                 145                 150
102 atc ggg atc ctc ggt gct tat ctt tct gat acc gcc ttc agc tac acc     533
103 Ile Gly Ile Leu Gly Ala Tyr Leu Ser Asp Thr Ala Phe Ser Tyr Thr
104                 155                 160                 165
106 ggt gca tgg cgc tgg atg ctg ggt gtg att atc atc ccg gca att ttg     581
107 Gly Ala Trp Arg Trp Met Leu Gly Val Ile Ile Ile Pro Ala Ile Leu
108                 170                 175                 180
110 ctg ctg att ggt gtc ttc ttc ctg cca gac agc cca cgt tgg ttt gcc     629
111 Leu Leu Ile Gly Val Phe Phe Leu Pro Asp Ser Pro Arg Trp Phe Ala
112          185                 190                 195
114 gcc aaa cgc cgt ttt gtt gat gcc gaa cgc gtg ctg cta cgc ctg cgt     677
115 Ala Lys Arg Arg Phe Val Asp Ala Glu Arg Val Leu Leu Arg Leu Arg
116 200                 205                 210                 215
118 gac acc agc gcg gaa gcg aaa cgc gaa ctg gat gaa atc cgt gaa agt     725
119 Asp Thr Ser Ala Glu Ala Lys Arg Glu Leu Asp Glu Ile Arg Glu Ser
120                 220                 225                 230
122 ttg cag gtt aaa cag agt ggc tgg gcg ctg ttt aaa gag aac agc aac     773
123 Leu Gln Val Lys Gln Ser Gly Trp Ala Leu Phe Lys Glu Asn Ser Asn
124                 235                 240                 245
126 ttc cgc cgc gcg gtg ttc ctt ggc gta ctg ttg cag gta atg cag caa     821
127 Phe Arg Arg Ala Val Phe Leu Gly Val Leu Leu Gln Val Met Gln Gln
128          250                 255                 260
```

Input Set : A:\Sequence Listing 81000.txt
Output Set: N:\CRF4\04062004\J812315.raw

```
130 ttc acc ggg atg aac gtc atc atg tat tac gcg ccg aaa atc ttc gaa        869
131 Phe Thr Gly Met Asn Val Ile Met Tyr Tyr Ala Pro Lys Ile Phe Glu
132     265                 270                 275
134 ctg gcg ggt tat acc aac act acc gag caa atg tgg ggg acc gtg att        917
135 Leu Ala Gly Tyr Thr Asn Thr Thr Glu Gln Met Trp Gly Thr Val Ile
136 280                 285                 290                 295
138 gtc ggc ctg acc aac gta ctt gcc acc ttt atc gca atc ggc ctt gtt        965
139 Val Gly Leu Thr Asn Val Leu Ala Thr Phe Ile Ala Ile Gly Leu Val
140                 300                 305                 310
142 gac cgc tgg gga cgt aaa cca acg cta acg ctg ggc ttc ctg gtg atg       1013
143 Asp Arg Trp Gly Arg Lys Pro Thr Leu Thr Leu Gly Phe Leu Val Met
144                 315                 320                 325
146 gct gct ggc atg ggc gta ctc ggt aca atg atg cat atc ggt att cac       1061
147 Ala Ala Gly Met Gly Val Leu Gly Thr Met Met His Ile Gly Ile His
148                 330                 335                 340
150 tct ccg tcg gcg cag tat ttc gcc atc gcc atg ctg ctg atg ttt att       1109
151 Ser Pro Ser Ala Gln Tyr Phe Ala Ile Ala Met Leu Leu Met Phe Ile
152     345                 350                 355
154 gtc ggt ttt gcc atg agt gcc ggt ccg ctg att tgg gta ctg tgc tcc       1157
155 Val Gly Phe Ala Met Ser Ala Gly Pro Leu Ile Trp Val Leu Cys Ser
156 360                 365                 370                 375
158 gaa att cag ccg ctg aaa ggc cgc gat ttt ggc atc acc tgc tcc act       1205
159 Glu Ile Gln Pro Leu Lys Gly Arg Asp Phe Gly Ile Thr Cys Ser Thr
160                 380                 385                 390
162 gcc acc aac tgg att gcc aac atg atc gtt ggc gca acg ttc ctg acc       1253
163 Ala Thr Asn Trp Ile Ala Asn Met Ile Val Gly Ala Thr Phe Leu Thr
164                 395                 400                 405
166 atg ctc aac acg ctg ggt aac gcc aac acc ttc tgg gtg tat gcg gct       1301
167 Met Leu Asn Thr Leu Gly Asn Ala Asn Thr Phe Trp Val Tyr Ala Ala
168         410                 415                 420
170 ctg aac gta ctg ttt atc ctg ctg aca ttg tgg ctg gta ccg gaa acc       1349
171 Leu Asn Val Leu Phe Ile Leu Leu Thr Leu Trp Leu Val Pro Glu Thr
172     425                 430                 435
174 aaa cac gtt tcg ctg gaa cat att gaa cgt aat ctg atg aaa ggt cgt       1397
175 Lys His Val Ser Leu Glu His Ile Glu Arg Asn Leu Met Lys Gly Arg
176 440                 445                 450                 455
178 aaa ctg cgc gaa ata ggc gct cac gat taa tctccccaag cttcctccc         1446
179 Lys Leu Arg Glu Ile Gly Ala His Asp
180                 460
182 <210> SEQ ID NO: 4
183 <211> LENGTH: 464
184 <212> TYPE: PRT
185 <213> ORGANISM: Escherichia coli
188 <400> SEQUENCE: 4
189 Met Pro Asp Ala Lys Lys Gln Gly Arg Ser Asn Lys Ala Met Thr Phe
190 1               5                   10                  15
192 Phe Val Cys Phe Leu Ala Ala Leu Ala Gly Leu Leu Phe Gly Leu Asp
193                 20                  25                  30
195 Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala Asp Glu Phe Gln
```

```
196         35                    40                    45
198 Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly
199     50                    55                    60
201 Ala Ala Val Gly Ala Val Gly Ser Gly Trp Leu Ser Phe Lys Leu Gly
202 65                    70                    75                    80
204 Arg Lys Lys Ser Leu Met Ile Gly Ala Ile Leu Phe Val Ala Gly Ser
205                   85                    90                    95
207 Leu Phe Ser Ala Ala Ala Pro Asn Val Glu Val Leu Ile Leu Ser Arg
208             100                   105                   110
210 Val Leu Leu Gly Leu Ala Val Gly Val Ala Ser Tyr Thr Ala Pro Leu
211         115                   120                   125
213 Tyr Leu Ser Glu Ile Ala Pro Glu Lys Ile Arg Gly Ser Met Ile Ser
214     130                   135                   140
216 Met Tyr Gln Leu Met Ile Thr Ile Gly Ile Leu Gly Ala Tyr Leu Ser
217 145                   150                   155                   160
219 Asp Thr Ala Phe Ser Tyr Thr Gly Ala Trp Arg Trp Met Leu Gly Val
220             165                   170                   175
222 Ile Ile Ile Pro Ala Ile Leu Leu Leu Ile Gly Val Phe Phe Leu Pro
223             180                   185                   190
225 Asp Ser Pro Arg Trp Phe Ala Ala Lys Arg Arg Phe Val Asp Ala Glu
226         195                   200                   205
228 Arg Val Leu Leu Arg Leu Arg Asp Thr Ser Ala Glu Ala Lys Arg Glu
229     210                   215                   220
231 Leu Asp Glu Ile Arg Glu Ser Leu Gln Val Lys Gln Ser Gly Trp Ala
232 225                   230                   235                   240
234 Leu Phe Lys Glu Asn Ser Asn Phe Arg Arg Ala Val Phe Leu Gly Val
235             245                   250                   255
237 Leu Leu Gln Val Met Gln Gln Phe Thr Gly Met Asn Val Ile Met Tyr
238             260                   265                   270
241 Tyr Ala Pro Lys Ile Phe Glu Leu Ala Gly Tyr Thr Asn Thr Thr Glu
242         275                   280                   285
244 Gln Met Trp Gly Thr Val Ile Val Gly Leu Thr Asn Val Leu Ala Thr
245     290                   295                   300
247 Phe Ile Ala Ile Gly Leu Val Asp Arg Trp Gly Arg Lys Pro Thr Leu
248 305 ·                 310                   315                   320
250 Thr Leu Gly Phe Leu Val Met Ala Ala Gly Met Gly Val Leu Gly Thr
251             325                   330                   335
253 Met Met His Ile Gly Ile His Ser Pro Ser Ala Gln Tyr Phe Ala Ile
254             340                   345                   350
256 Ala Met Leu Leu Met Phe Ile Val Gly Phe Ala Met Ser Ala Gly Pro
257         355                   360                   365
259 Leu Ile Trp Val Leu Cys Ser Glu Ile Gln Pro Leu Lys Gly Arg Asp
260     370                   375                   380
262 Phe Gly Ile Thr Cys Ser Thr Ala Thr Asn Trp Ile Ala Asn Met Ile
263 385                   390                   395                   400
265 Val Gly Ala Thr Phe Leu Thr Met Leu Asn Thr Leu Gly Asn Ala Asn
266             405                   410                   415
268 Thr Phe Trp Val Tyr Ala Ala Leu Asn Val Leu Phe Ile Leu Leu Thr
269             420                   425                   430
```

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/812,315**

DATE: 04/06/2004
TIME: 10:51:23

Input Set : **A:\Sequence Listing 81000.txt**
Output Set: **N:\CRF4\04062004\J812315.raw**

```
271 Leu Trp Leu Val Pro Glu Thr Lys His Val Ser Leu Glu His Ile Glu
272         435             440             445
274 Arg Asn Leu Met Lys Gly Arg Lys Leu Arg Glu Ile Gly Ala His Asp
275     450             455             460
```

VERIFICATION SUMMARY   DATE: 04/06/2004
PATENT APPLICATION: **US/10/812,315**   TIME: 10:51:24

Input Set : **A:\Sequence Listing 81000.txt**
Output Set: **N:\CRF4\04062004\J812315.raw**

```
L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:37 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:52 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:61 M:283 W: Missing Blank Line separator, <400> field identifier
```